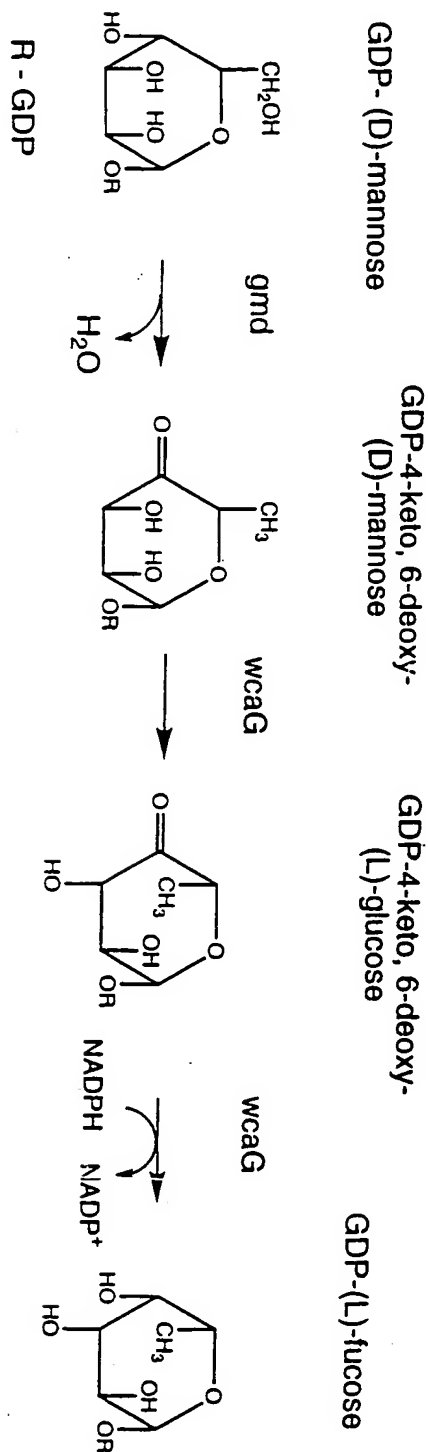


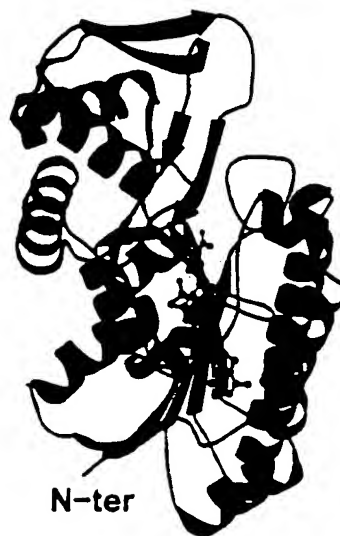
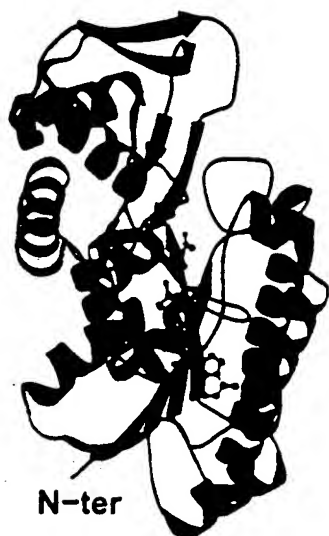


CRYSTAL STRUCTURE OF E. COLI GDP-FUCOSE SYNTHETASE  
(AND COMPLEXES THEREOF) AND METHODS OF IDENTIFYING  
AGONISTS AND ANTAGONISTS USING SAME



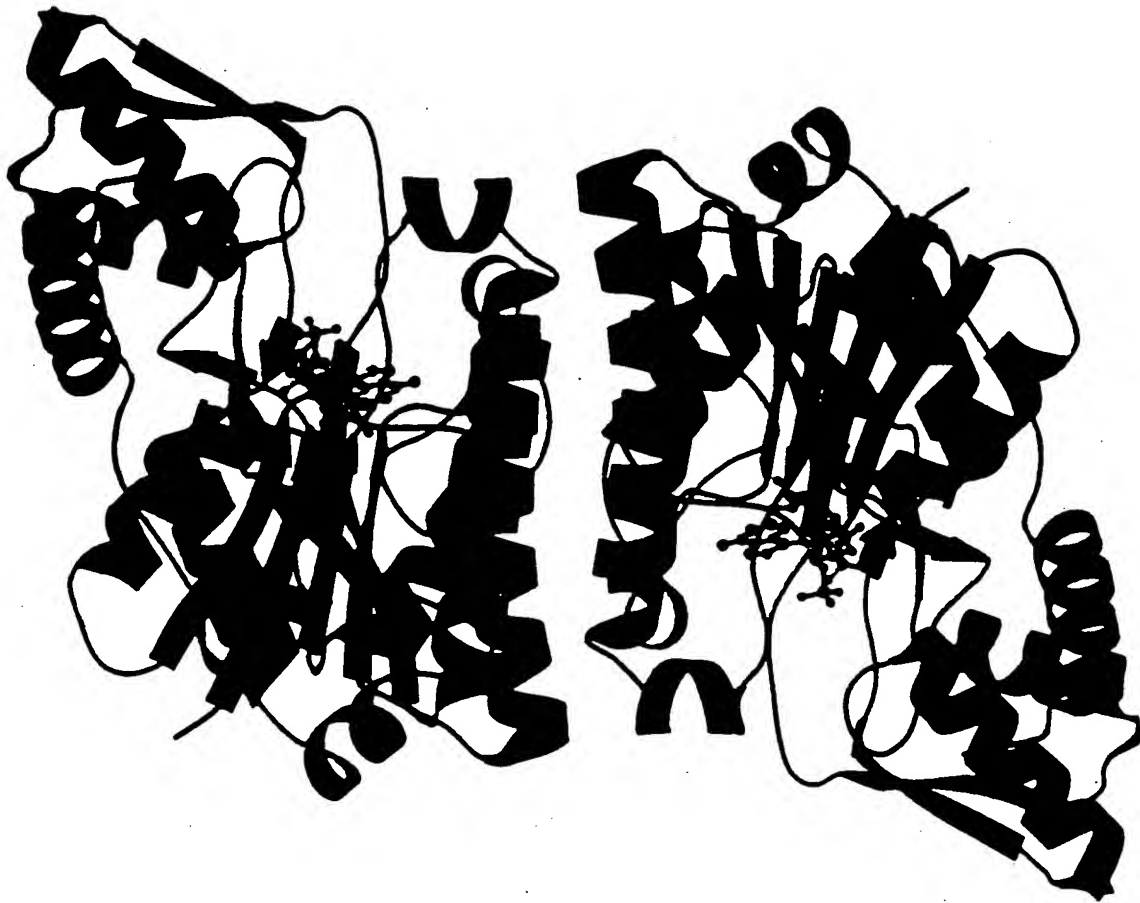


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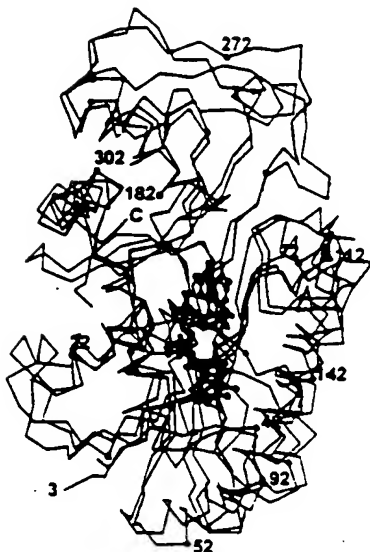


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```
gale      1  -MRVLVTSGYIGSHTCVQLONG-HDVIIIDNLC KRSVLPVIERLGGKEPTFVEGD
coli_GFS  3  KQRFVFIAGHGEVGSATRRQLEQNGDVIELVLRTR-----DELN
human_GFS  8  -MRILVTGSGSLVCKATQNVVADCAQLPGEDWVF-----VSSKDAD
consensus 1  .....

gale      59  IRNEALMTIELHDHAIDTVIHTAGLKA-VGESVQKPLEYDNNVNGTLRLTSAMRAAMVK
coli_GFS  41  LLDGRAVHDFEASERIDQVYLAARVCGIVANNTPADSTYQNHMHESNLIHAHQNDVN
human_GFS  48  LTDTAQTRALPEKVQPTHVHLAAEVGGLFRNKKYNLDGWRKNVENDNVLHSAFEVGAR
consensus 61  .....

gale      118  NFIESSSATVVGCDNPKIPYVES-FPTGTETQ---SPYCKSKLEVEQHLTDLQKAQPDWSIA
coli_GFS  101  KLLPLGSSCIYPKLARQPMASEELQGTLEPTNEPYATKLAGIKCESYNRCY-GRDYR
human_GFS  108  KVVSLSTCIPFDKTTYPIDEYMHENGPPHNSFGYSYARRMIDVQNRAYQOY-GCTET
consensus 121 .....

gale      174  LERYFNPFVGAHPSGDMGEDPQGIFFNNLEBYIAQVAVGR----RDSLAIEGNDYPTEDGTG
coli_GFS  160  SVMPTNLYGPH-----DNFHPNSSEVIPALLRRFDEATAQNAFDVVVWGS-----GTF
human_GFS  167  AVIPTNVFGPHDNF-----NIEDGHVLEGLIHRVELAKS-SGSALTVMGTC-----NE
consensus 181 .....

gale      230  VRDYIHVMDLADGHVVAHEKLANK-----EGVETYNLGAGVCHSVLDVVAATSKACGKP
coli_GFS  208  HREPLHVDDMAASHEVMELEAEVWLENTQPMLSHINVGTGVDCITIRELAQTHARVVGK
human_GFS  214  RROFIYSLDLAQLFWVIREYNE-----VEPIILSVGEEDSVSIKAAAEAVVEAMDEH
consensus 241 .....

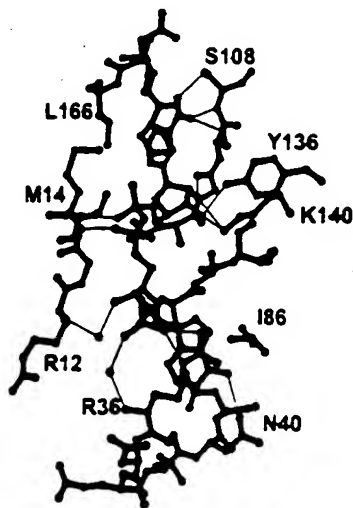
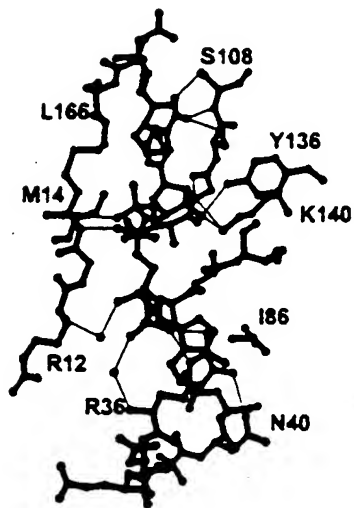
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coli_GFS  268  GRVVPDASKPDGTPRKLLDVRLHQ-LGWYHEISLEAGLASTYQWFLENQDRF
human_GFS  267  GEVTFDTTRSDGQPKKTASNSKLRTYLPDERFTPFKQAVKETCAWFTDNYEQARK
consensus 301 .....
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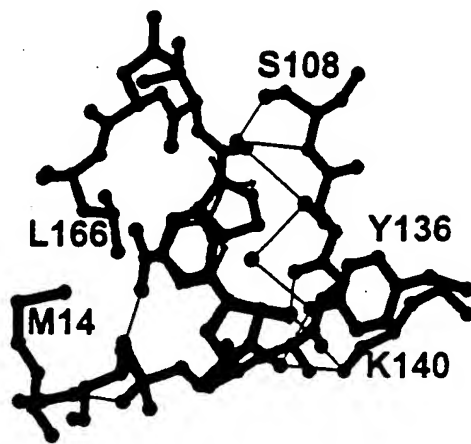
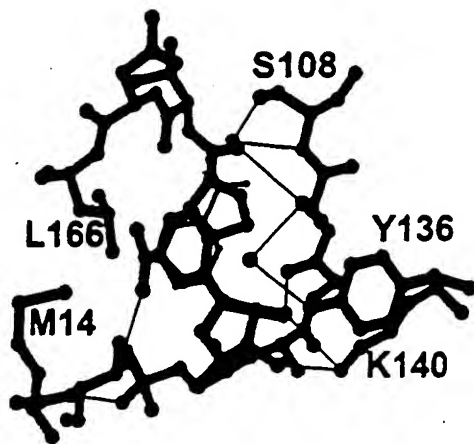


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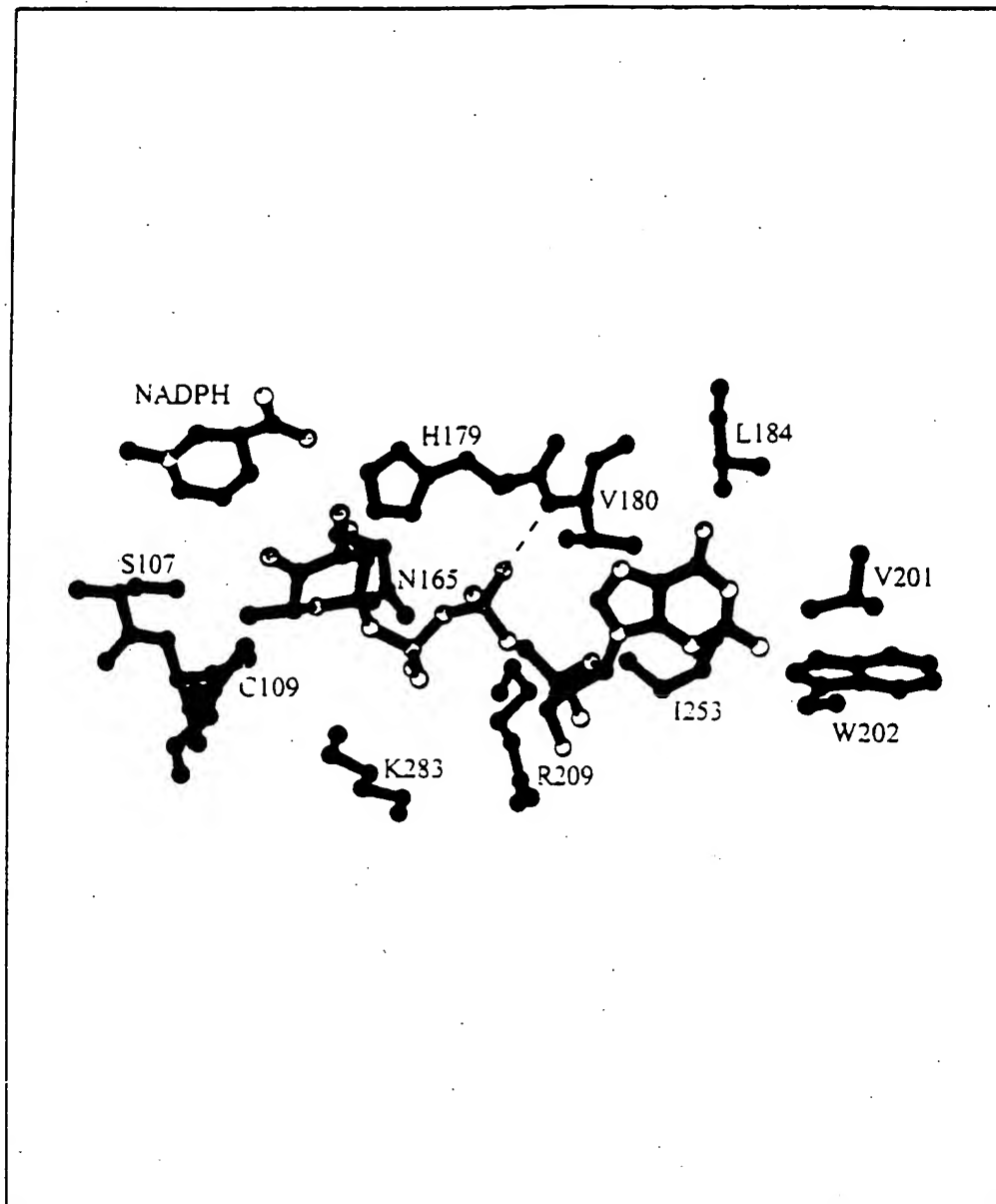
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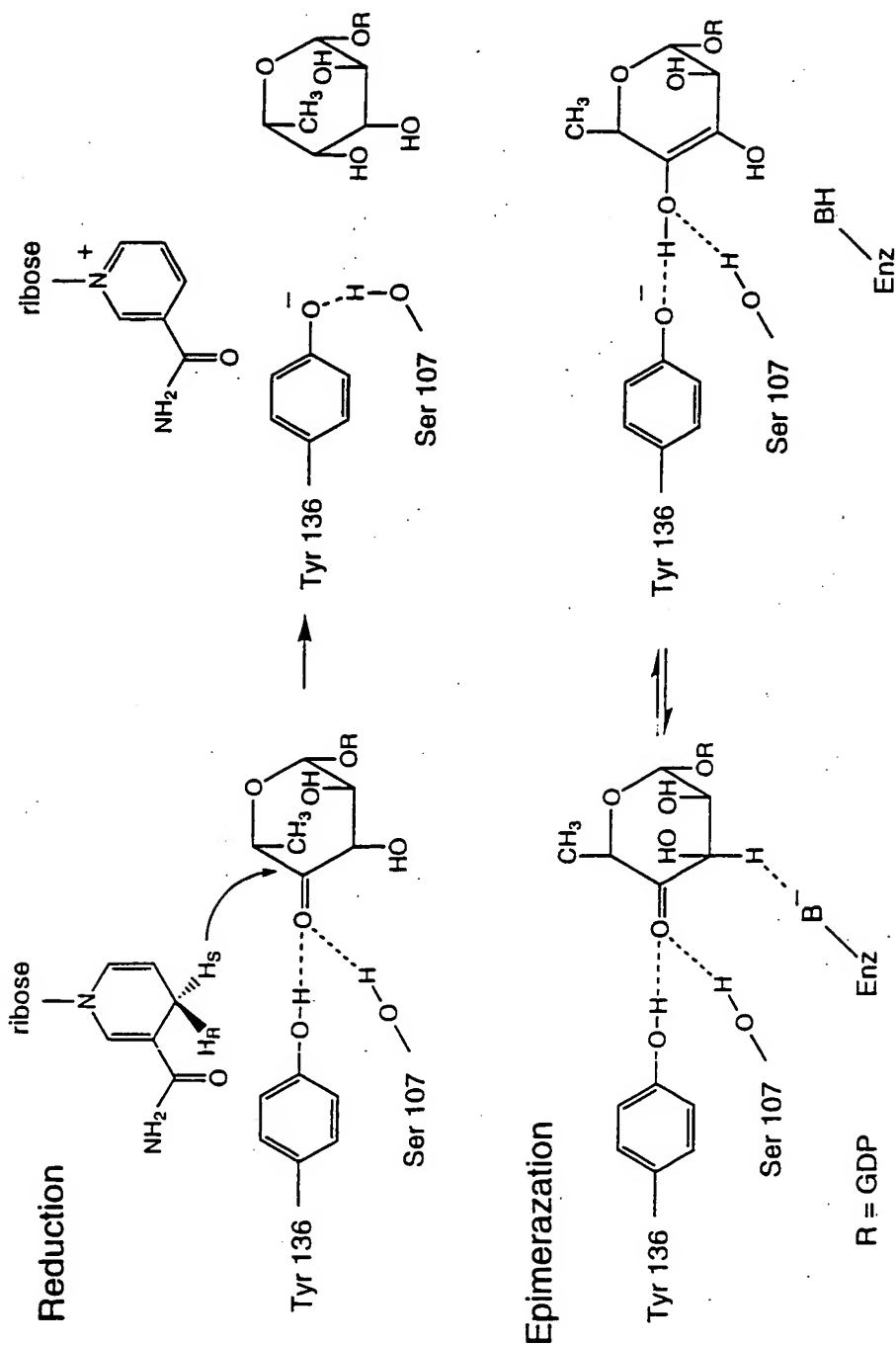




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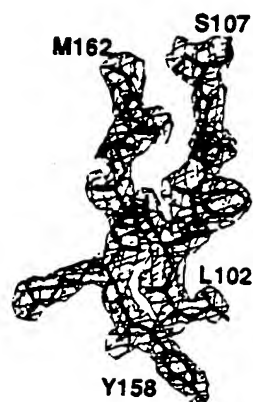


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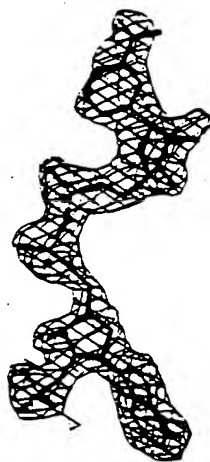


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